

## First record of the genus *Phyllorhiza* spp. (Cnidaria; Scyphozoa, Mastigiidae) in the coastal waters of Malaysia

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### Abstract

This study employed two mitochondrial markers, 16S rRNA and cytochrome c oxidase I (COI) for species identification and resolved the taxonomic and systematic as well as population genetics of *Phyllorhiza* spp. in the coastal waters of Malaysia. A total number of 65 individuals sampled from three locations representing the three regions fringing the coastline. Phylogenetic trees constructed using Mega 5.0 software and Kimura 2-parameter with 1000 bootstrap replication were used to test reliability. The molecular data in complement with morphological differentiation revealed, at least three different species for the genus *Phyllorhiza*, *Phyllorhiza punctata* inhabit the coasts of Peninsular Malaysia while *Phyllorhiza* sp.2 and *Phyllorhiza* sp.3 which were only observed in East Peninsular Malaysia. The results of the current study also highlighted that colour alone is not sufficient for species differentiation of *Phyllorhiza* spp. The blue morphotype of *Phyllorhiza* sp.1 observed in East Peninsular Malaysia was genetically identical to the brown morphotype observed in Northwest of Peninsular and recognised as *P. punctata* while the presence of *Phyllorhiza* sp.2 and *Phyllorhiza* sp.3 have never been recorded before in Malaysia. Consequently, understanding the taxonomy of local and invasive jellyfishes are necessary requirements for their management.

**Key words:** *Phyllorhiza* spp.; Mitochondrial markers; Jellyfish; Malaysia.

### 1. Introduction

Every year new invasive animals are reported in the marine ecosystems (Bax *et al.*, 2003). Invasive species are generally defined as foreign species whose introduction does or likely to cause economic or

environmental harm to human health. Actually, any species removed from its native range has the potential to become invasive due to within its normal range predation, disease, parasite, competition, and other natural controls acts to keep population levels in check. If released from this controls, species

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abundance have the potential to reach levels that interfere with or displace local fauna such effect may occur immediately, depends on the characteristics of the individual species and the conditions into which it is introduced it may be never realized at all or accrued after some period of delay (Ray, 2005b). Phytoplankton has an important link in the food chain; they are agent for primary production and through the process of photosynthesis they abtain energy. An invasive species can lead to a disappearance and reduction in phytoplankton availability and consequently affect a marine ecosystem food web resulting in reduced zooplankton and fish abundance and changed feeding habits of resident fish (Ray, 2005a).

*Phyllorhiza punctata* Von Lendenfeld, 1884 is a well known invasive Scyphomedusae belonging to the order of Rhizostomeae and family of Mastigiidae and indigenous to the tropical western Pacific and have successfully migrated globally (Graham *et al.*, 2003; Ray, 2005a). Prior to 1950, this species was the only known in the Indo-Pacific Ocean. Today it has been documented in many locations of the world wide such as Gulf of Mexico (Graham *et al.*, 2003; Chilton *et al.*, 2011), Southern Aegean coast of Turkey (Gülşahin and Tarkan, 2012), Italian waters, west of Mediterranean Sea (Boero *et al.*, 2009), and the coastal waters of Brazil (Haddad and Nogueira Júnior, 2006).

*Phyllorhiza punctata* prey upon many economically important organisms, including crustaceans, bivalve larvae, and fish eggs and larvae, within their native range resulting in negative effects on the economy and ecology of the marine ecosystems (Chilton *et al.*, 2011). For example, Graham *et al.* (2003) reported, indirect evidence that the presence of *P. punctata* in the Gulf of Mexico decreased the total catch of white shrimp (*Litopenaeus setiferus*) in Mobile Bay, Alabama and Mississippi Sounds by 27% (clogging of nets, damage to boat intake and fishing gear and area closures).

Several aspects of this invasive species have been investigated in the literature. These encom-

pass; detailed morphology (Mayer, 1910; Kramp, 1961), reproduction and survival (Rippingale and Kelly, 1995), behaviour and prey capture (D'ambra *et al.*, 2001), and the population dynamics and production of *P. punctata* in Laguna Joyuda (Joyuda and Rico, 1990). *P. punctata* has large size with a characteristic colouration and inhabits the upper layer of the water. The living specimens are brown with obvious white spots and have eight radial canals, the bell diameter varies between 2-470 mm and the weight ranged between 0.26-3882.2g (Haddad and Nogueira Júnior, 2006). Sim (2009) and Chuah (2012) reported its occurrence in Malaysia based on morphological traits.

*Phyllorhiza* is an efficient invasive organism that caused immense damage in marine ecosystem. Very limited genetic information is available for the taxonomy and classification of this genus and to date, no published data recorded regarding the molecular taxonomy of this important species in Malaysia. There has been complication in distinguishing between *Phyllorhiza* and another genus, *Mastigias* which also a member of the family Mastigiidea. Stiasny (1924) first reported the genetic description of these two genera, although some confusion had remained. Similarly, another species, *M. albipunctatus* identified from Jamaican waters (Vannucci, 1964) was also regarded a likely misident. Bayha and Graham (2011) confirmed the presence of the *Mastigias* in the Atlantic basin and suggested that the origin of this genus may be in the central Indo-Malayan region. According to Dawson and Jacobs (2001) molecular genetics techniques can facilitate determination of species boundaries as well as correcting morphological misidentifications. Thus, its management is critical and the investigation of the taxonomy and genetic population of the genus *Phyllorhiza* is a prerequisite for formulating strategies to achieve this. The data would be an important contribution towards the management of this group, which is fast becoming an unwelcome and sometimes deadly feature, in many global waters in the past recent years. The current study

discerns the characters of genetic diversity, phylogenetic and phylogeography among the populations inhabiting the Peninsular Malaysian waters.

## 2. Materials and methods

Seven morphotypes of *Phyllorhiza* spp. collected from three populations: 1. Muka Head, Penang

Island, 2. Langkawi Island in (Northwest), and 3. Kuala Terengganu (East) (with all three located in Peninsular Malaysia) from November 2010 to September 2011 (Figure 1, Table 1). Two methods were used for sampling; the push net (scoop nets) for the specimens from the surface and towing methods in deeper waters specimens. The specimens from Kuala Terengganu obtained from fishermen.

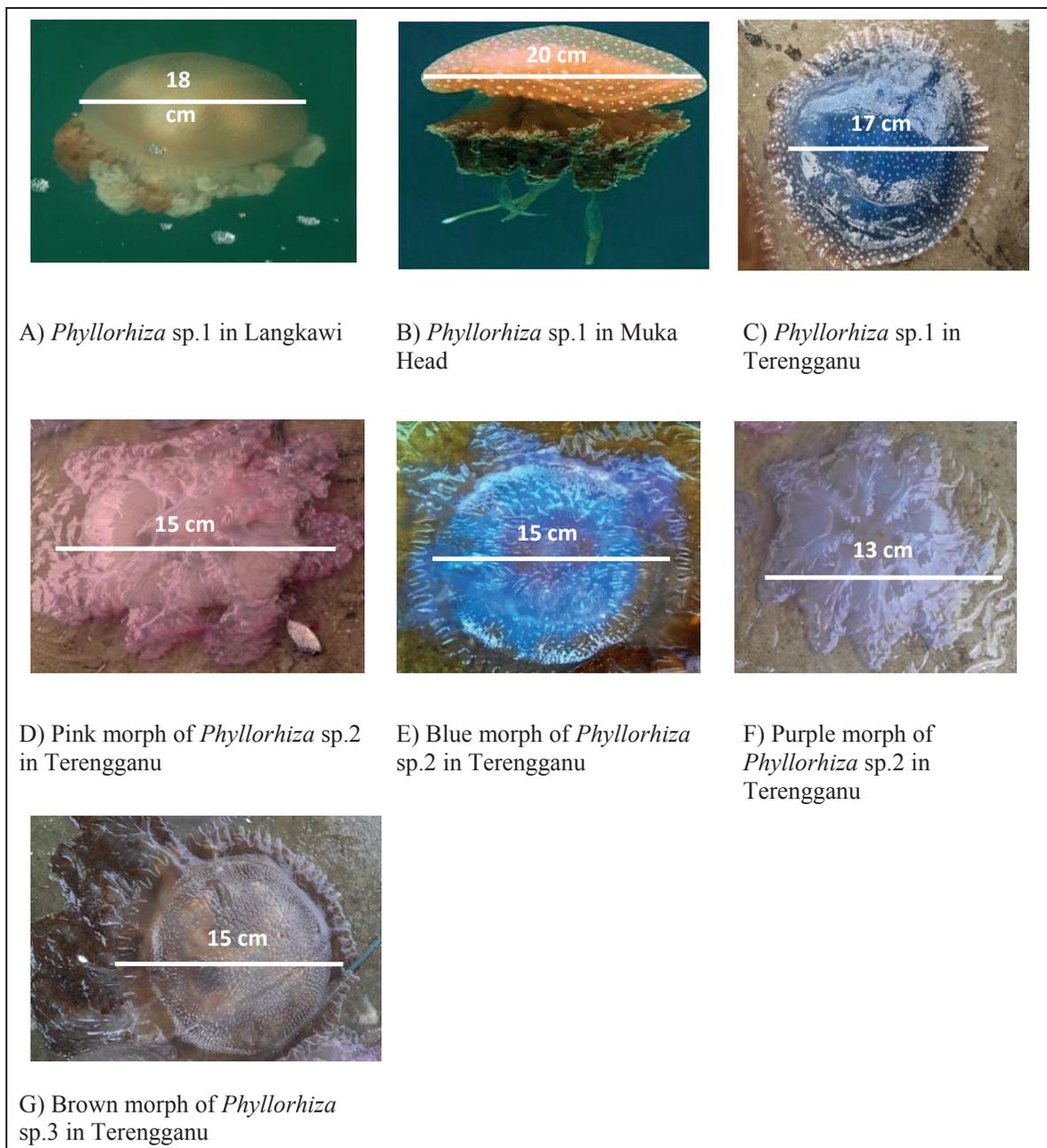


Figure 1. Different morphotype of *Phyllorhiza* spp. (A-G)

Table 1. Sampling site, tag label, number of morphological types, sample size, sampling date and GPS coordinates of *Phyllorhiza* spp. populations investigated along the Malaysian coast

	Location and Tag	Region	No. of Morphological Types and samples		Sampling Date	Location Coordinate
1	Penang (MH)	Northwest Peninsular	1	20	Nov 2010	5°24'00"N100°14'20"E
2	Langkawi (L)	Northwest Peninsular	1	20	Nov 2010	6°21'N 99°48'E
3	Terengganu (T)	East Peninsular	5	25	Sep 2011	5°20'0"N103°9'0"E

These specimens identified as *Phylloriza* according to Mayer (1910) and Kramp (1961) key, but even within each presumed species colour variations occurred. Total genomic DNA of 65 specimens were extracted using AQUAGENOMIC™ kit (Multi Target Pharmaceuticals, Salt Lake City, Utah 84116), following the manufacturers' protocol. The target genes, 16S rRNA was amplified using specific Cnidaria primers (Bridge *et al.*, 1992), while cytochrome c oxidase I (COI) was amplified based on universal primers by Folmer (1994), and Bayha (2005). PCR products were purified using PROMEGA kit (Wizard Purification Systems). This was to ensure removal of unincorporated primers, nucleotides, polymerases and salts. An electrophoresis run on a 2% (w/v) agarose gel conducted to detect satisfactory PCR products. These products were sequenced on an ABI3730XL Genetic Analyser (Applied Bio systems). Multiple DNA sequences were edited, and aligned using Mega 5 software (Tamura *et al.*, 2007). Intrapopulation and interpopulation diversity within morphotypes and genetic distance between them were estimated based on Kimura 2-parameter (Kumar *et al.*, 2004). Collapse 1.2 was used to obtain unique haplotype sequences. No GenBank vouchers were available for *Phylloriza* spp. *Mastigias* sp. Bayha (2011- JN215547.1, JN215548, JN215549.1, JN215550.1 and N215551.1 from Atlantic Ocean, *M. papua Gotoh* (2012- AB720919.1 from Japan), *Cyanea capillata* and *Catostylus mo-*

*saicus*, Kayal (2012- JN700937.1, JN700940.1 from USA) *Cassiopea* sp. Bridge (1995- U19374.1 from USA) and *Nemopilema nomurai* Zhang (2008- EU373727.1 from China) used as a outgroups for comparisons in geographic distance analysis in 16S rRNA gene. Unfortunately, amplification of *Phyllorhiza* spp. for COI gene was unsuccessful even after several optimisation attempts and using different primers.

### 3. Results

Several morphological parameters from different morphotypes of *Phyllorhiza* spp. are presented in Table 2. Common characteristics of all four *Phyllorhiza* spp. morphotypes confirmed these species based on their morphological characteristic belongs to the *Phyllorhiza* spp. and different with other jellyfish species. Sixty-five individual's sequences of the 16S rRNA gene were successfully amplified and the lengths of amplicons were 700bp base pairs. The lengths of amplicons in 16S rRNA gene were 700bp base pairs. The frequencies of observed transitions and transversions of 16S rRNA gene increased linearly with increasing genetic distance (Kimura 2-Parameter). This suggested that the aligned sequences had no marked saturation effects and therefore were suitable for phylogenetic analysis.

Table 2. Morphological characteristics of *Phyllorhiza* spp. in the coastal waters of Malaysia

<b>Morphological characteristics</b>	
Common characteristics of all four <i>Phyllorhiza</i> spp morphotypes	
Bell Shape	Mushroom shaped bell, Nearly hemispherical, radially symmetrical
Surface texture of bell	Smooth and soft
Presence of bell edge marginal tentacles	Yes
Bell section (septa)	Octant (eight sections)
Number of oral arms and shape of oral arms	Four , Thick semi transparent highly dichotomous oral
Colour variation in different morphotypes of <i>Phyllorhiza</i> spp. (Pattern mark)	
<i>Phyllorhiza</i> sp.1	Brown and blue. White dots interspersed around the bell. This fits the description of <i>Phyllorhiza punctata</i> as according to the morphological keys of Kramp (1961).
<i>Phyllorhiza</i> sp.2	Blue, pink, and purple, without white dots interspersed around the bell.
<i>Phyllorhiza</i> sp.3	Dark brown, without dots interspersed around the bell.

The intra-species and interspecies (intra-genera) genetic distances, calculated based on Kimura 2-Parameter, are shown in Table.3. Related sequences from GenBank were included and BLAST analysis conducted to compare and identify the specimens where possible.

Table 3: Intra and interspecies /morphotype genetic distance based on Kimura 2-parameter of 16S rRNA gene in *Phyllorhiza* spp.

	1	2	3	4	5	6	7	8	9	10	11	12	13
1 <i>Phyllorhiza</i> sp.1 MH	0.00												
2 <i>Phyllorhiza</i> sp.1 L	0.02	0.02											
3 <i>Phyllorhiza</i> sp.1 T	0.02	0.03	0.00										
4 <i>Phyllorhiza</i> sp.2 blue	0.20	0.20	0.21	0.00									
5 <i>Phyllorhiza</i> sp.2 pink	0.20	0.20	0.21	0.00	0.00								
6 <i>Phyllorhiza</i> sp.2 purple	0.20	0.20	0.21	0.00	0.00	0.00							
7 <i>Phyllorhiza</i> sp.3 T	0.18	0.19	0.19	0.23	0.23	0.23	0.07						
8 <i>Mastigias</i> sp. Atlantic JN215547.1- 51.1	0.15	0.16	0.16	0.23	0.23	0.23	0.23	0.00					
9 <i>Mastigias papua</i> Japan AB720919.1	0.15	0.16	0.16	0.23	0.23	0.23	0.23	0.00					
10 <i>Cassiopea</i> sp. USA U19374.1	0.21	0.21	0.22	0.25	0.25	0.25	0.23	0.21	0.21				
11 <i>Cyanea capillata</i> USA JN700937.1	0.35	0.35	0.35	0.36	0.36	0.36	0.36	0.34	0.27	0.23			
12 <i>Catostylus mosaicus</i> USA JN700940.1	0.28	0.28	0.28	0.31	0.31	0.31	0.28	0.25	0.25	0.23	0.33		
13 <i>Nemopilema nomuria</i> China EU373727.1	0.27	0.28	0.27	0.28	0.31	0.31	0.30	0.27	0.28	0.26	0.30	0.26	

The *Phyllorhiza* sequences are new records as no GenBank sequence has been previously reported for this genus, and their identification in previous studies had been solely based on morphology. The 16S rRNA data revealed that the range of intraspecies (interpopulation) for each morphotype was 0.00-7%. Intrapopulation distance in *Phyllorhiza* sp.1 was 0.00-2 %, of similar in magnitude as the interpopulation distance of 2-3%. No genetic variation (0.000) was observed within and between morphotypes of *Phyllorhiza* sp.2, which were only found in Kuala Terengganu. *Phyllorhiza* sp.3 which

was also only found in Kuala Terengganu had the highest intraspecies variation of 7% although found only in a single population. The range of interspecies (intragenera) values within *Phyllorhiza* was 18–23%. The *Phyllorhiza* sp.1-sp.3 pairwise comparison was the lowest at 18 % while *Phyllorhiza* sp.2- sp.3 was the highest at 23%. Analysis of the interspecies variation revealed one interesting observation- the closeness of *Mastigias* sp. and *M. papua* to *Phyllorhiza* especially to *Phyllorhiza* sp.1 of 15-16% genetic distance. This was even lower than the divergence between the two most closely

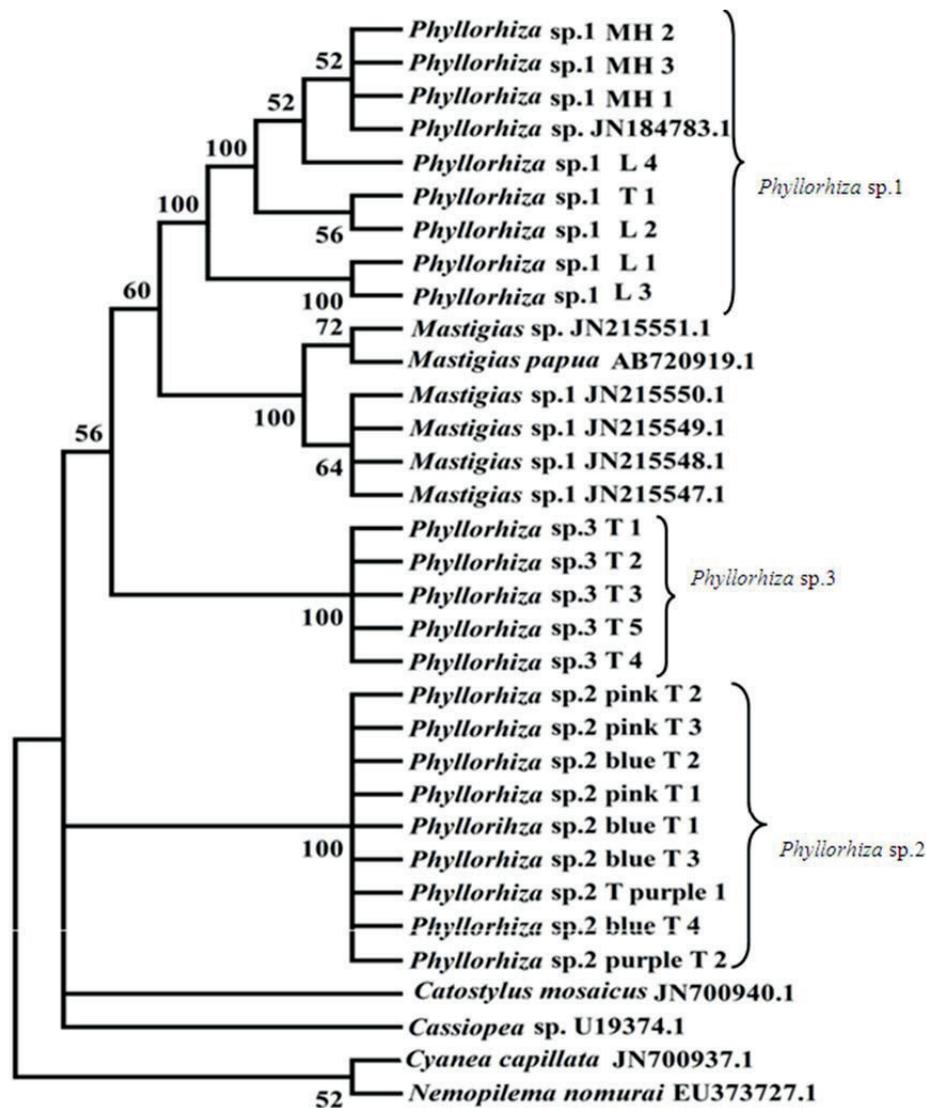


Figure 3. Neighbour Joining Phylogenetic tree of *Phyllorhiza* spp. in Malaysian waters based on Kimura 2 parameters of 16S rRNA gene with 1000 bootstrap replication. The scale bar is corrected distance (k2-P=0.02)

related *Phyllorhiza* (*Phyllorhiza* sp.1- sp.3) pair of 18%. In addition, *Mastigias* vouchers' from USA and Japan were homogeneous with no genetic variation observed for 16S rRNA gene. Among the *Phyllorhiza* spp and other outgroups (excluding *Mastigias*), the genetic distance ranged from 21% to 36%, the closest relationship was with *Cassiopea* sp. of 21% although from different genera. Among outgroups, genetic distances were also of the same magnitude for different genera.

The Neighbour-Joining tree is presented in

Figure.3. GenBank voucher sequences; *Mastigias* sp. (JN215547.1, JN215548.1, JN215549.1, JN215550.1 and JN215551), *Mastigias papua* (AB720919.1), *Cyanea capillata* (JN700937.1), *Phyllorhiza* sp. (JN184783.1), *Catostylus mosaicus* (JN700940.1), *Nemopilema nomurai* (EU373727.1) and *Cassiopea* sp. (U19374.1) were included as outgroups to clarify taxonomy of the *Phyllorhiza* and assess relationships with other taxa. Support at nodes are only presented for those with bootstrap values  $\geq 50\%$ . All clusters grouping

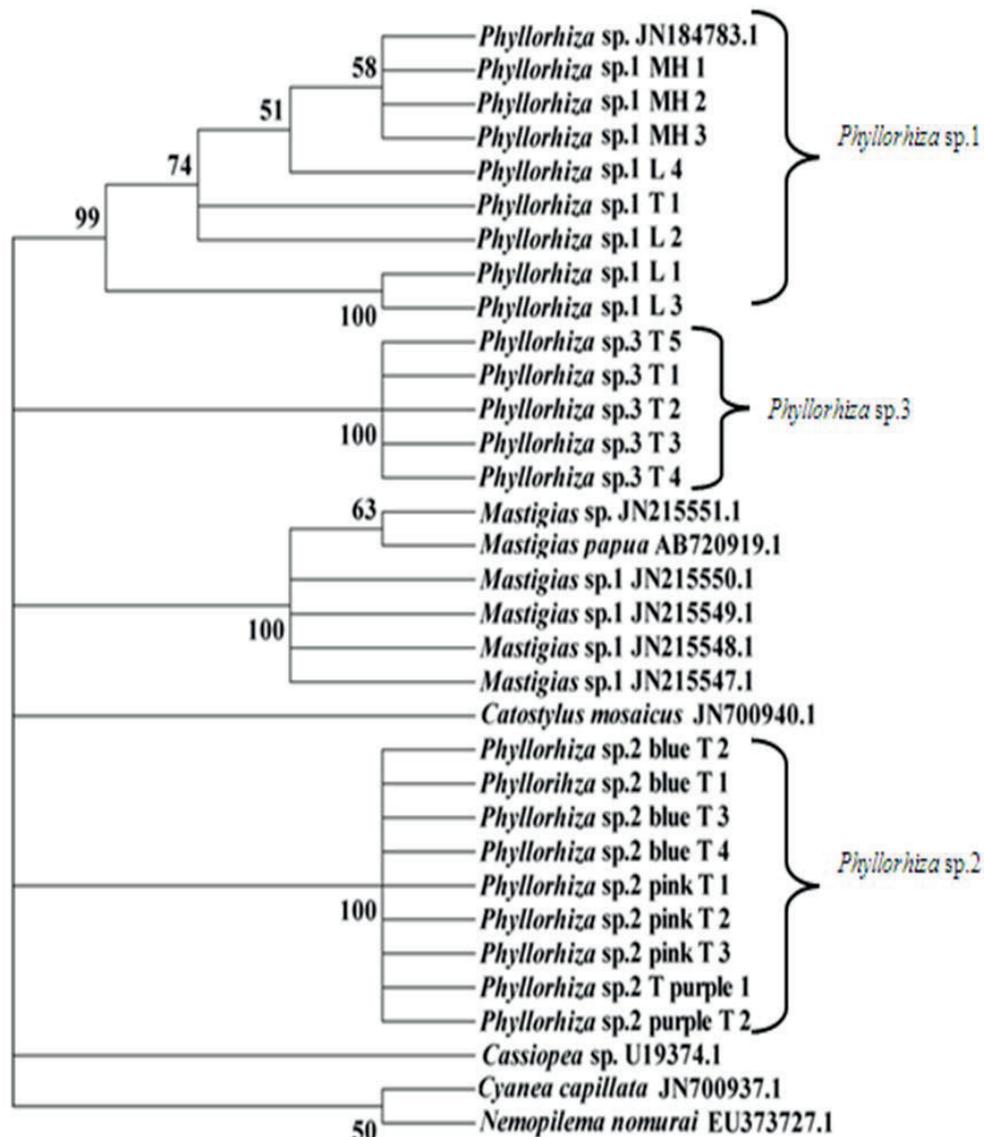


Figure 4. Maximum Likelihood Phylogenetic tree of *Phyllorhiza* spp. in Malaysian waters based on Close-Neighbour-Interchange (CNI) of 16S rRNA gene with 1000 replications

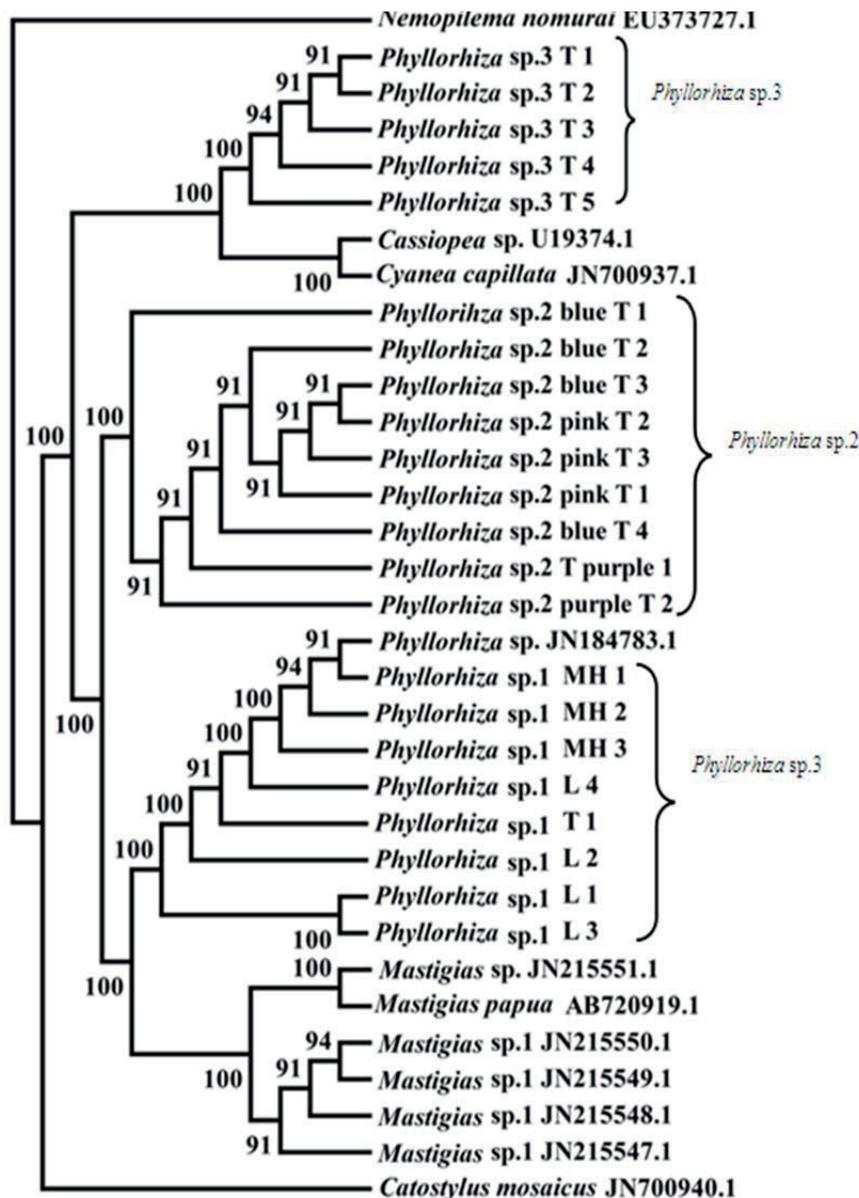


Figure 5. Maximum Parsimony Phylogenetic tree of *Phyllorhiza* spp. in Malaysian waters based on CNI of 16S rRNA gene with 1000 replications

each *Phyllorhiza* presumed species were very well supported 100 % confirming monophyly of each presumed species as identified by the 16S rRNA sequences but support at basal nodes were weak. To date, no GenBank sequence has been reported for this genus, and the analyses had been exclusively based on morphology. Three major clusters were formed with low support for their inter-relationship. The first cluster bifurcated into two well supported sub-clusters and was made up *Phyllorhiza* sp.1, all

from Northwest Peninsular and surprisingly another sub-cluster comprising of *Mastigias*, in agreement with the genetic distances described earlier. The second cluster consisted of *Phyllorhiza* sp.3 and formed the sister group to the first cluster and third cluster consisted of the different morphotypes of *Phyllorhiza* sp.2. All outgroup sequences formed the basal cluster.

The Maximum Likelihood (ML) and Maximum Parsimony (MP) tree of the partial 16S rRNA gene

are presented in Figures 4 and 5, which the trend and tree topology were similar to NJ analysis. However, in MP tree, the clustering at both terminal and basal nodes were well-supported and taxonomic relationships better resolved. Thus, in agreement with the NJ tree, all *Phyllorhiza* presumed species were monophyletic.

#### 4. Discussion

The current study highlights the dearth of information prevailing in the taxonomic data of the jellyfishes particularly in molecular aspects. While sequence data are available for the COI gene, no previous data on 16S rRNA gene is available for the genus *Phyllorhiza*. This had been the major limitation in fully resolving the taxonomic status of the investigated group, namely *Phyllorhiza*. Specifically, a few problems happened during the study to achieve the outlined objectives. Firstly, amplification of the COI gene for *Phyllorhiza* spp. was unsuccessful even after several optimisation attempts and utilisation of various primers. Secondly, as earlier mentioned, no published sequence data of 16S rRNA gene was available to support or refute the conclusion that the investigated specimens were *Phyllorhiza* spp. and that *Phyllorhiza* sp.1 was actually *Phyllorhiza punctata*.

Therefore, due to these limitations, two strategies were presented. The first one was to confirm with other workers and expertise, both local and foreign, of the morphological identity of the specimens. Having confirmed their morphological status, the second strategy was to compare the sequence divergence of the presumed *Phyllorhiza* spp. with other jellyfish species. Schroth *et al.* (2002) suggested a range of 5-32% for interspecific divergence for 16S rRNA gene. Collins *et al.* (2005) proposed a range of 5.4-48.6% divergence value for hydrozoan species. In another study, Bayha (2005) reported the range of 9.2-21.1% for a known species of *Chrysaora*. With the exception of three species of *Chrysaora* namely *C. fuscescens*, *C. achlyos* and

*C. colorata* from the Pacific Ocean which showed values of 1.4- 4.6%, any pair-wise value lower than the aforementioned is indicative of intraspecific relationship. In the current study, the intraspecific variation for 16S rRNA gene was 2-7% for each presumed species while the interspecific variation among them was 18-23%. Thus, it concluded that there were three valid species among the specimens investigated.

Comparatively, large morphological difference may accrue rapidly despite little genetic divergence variation in commonly assayed markers (Dawson, 2005). In contrast, relatively little morphological variation may sometimes be associated with deep genetic divergence (Dawson and Jacobs, 2001). Both phenomena were illustrated in this study where different colour variants of *Phyllorhiza* sp.1 showed lack of genetic divergence while high divergence were observed in *Phyllorhiza* sp.3. The present data is comparable with Holland *et al.* (2004) who reported deep divergence (20.3%) for populations of *Cassiopea* spp. in Hawaiians waters that were morphologically the same. He suggested that this high genetic distance may be indicative of ecological difference at their sources. Geographic overlap of different genotypes connected with fine-scale ecological division, reported in Aurelia and *Mastigias* (Dawson and Jacobs, 2001; Dawson, 2003). Consequently, they suggested that local adaptation may have led to ecological speciation.

The study based on morphology and molecular analyses provided preliminary results that the morphospecies of the Malaysian *Phyllorhiza* delineated into molecular species. The blue morphotype of *Phyllorhiza punctata* observed in East Peninsular Malaysia was genetically identical to the brown morphotype observed in Northwest Peninsular. *Phyllorhiza* sp.2 and *Phyllorhiza* sp.3 never been recorded before in Malaysia. Based on the present genetic data (Tables 3) and previous studies, morphological variation commonly observed for many species in this family, a few colour morphotypes were observed in a single presumed species. These

results were comparable with the closely related *M. papua* investigated in Palua Micronesia that were vastly different morphologically but were genetically indistinguishable (Dawson, 2005).

Bolton and Graham (2004) also reported similar range of colour variations for *Phyllorhiza* species and suggested that the presence of symbiotic zooxanthellae led to the polymorphic colour variation. Similarly, Ocaña Luna *et al.* (2010) theorized that colour might indicate the presence of zooxanthella in the tissue. In another study, Galil *et al.* (2009) observed pale or dark blue colour variation morphs for this species in the Israeli waters. Pigliucci (2001) explained that phenotypic plasticity is common in the organisms that are adaptive to new environmental conditions that account for observed diversity. Thus, this study furnish additional support that colour alone is not sufficient for species differentiation in the genus *Phyllorhiza*. In the case of *Phyllorhiza* sp.3 the reverse was observed in only one colour of morphotype (brown in colour but different from the brown morphotype of *Phyllorhiza* sp.1) although the genetic divergence overlapped into the lower end of interspecies boundaries despite all individuals being from a single population.

However, about the taxonomic identification of these three newly discovered or new records of species, the morphological identification of *Phyllorhiza* sp.1 was in agreement with morphological keys for *Phyllorhiza punctata* (Mayer, 1910; Stiasny, 1924; Kramp, 1961), and confirmed in consultation with local and foreign experts through specimen vouchers and photographs.

On the other hand, questions remained why interspecific distance between *Phyllorhiza* sp.1 with *Mastigias* (15-16%), although both formed distinct monophyletic groups, they were lower than with the other two presumed Malaysian *Phyllorhiza* species (18-23%). Based on the strength of available data from this and other studies, the ambiguities may lie on the taxonomic validity of GenBank *Mastigias* and not the conclusion of the present study. The first line of argument is that the phylogenetic

trees clustered the GenBank *Mastigias* within the *Phyllorhiza* cluster of the three presumed species, suggesting that the former is a member of the genus *Phyllorhiza*.

The second is that the occurrence of *Phyllorhiza* has never been reported in Malaysia but admittedly, this does not negate the fact that it could be a new record. The third is that the previously deposited GenBank sequences of *Mastigias* spp. from Japan and the Atlantic Ocean showed no genetic divergence (0.00%), a clear evidence that although the GenBank *Mastigias* sequences (which had been misidentified) most likely belonged to the genus *Phyllorhiza* and they are distinct species (15-16% genetic distance).

Stiasny (1924) stabilized the genetic definitions of *Phyllorhiza*, and *Mastigias*, but taxonomic ambiguities between these two genera have been of considerable debate until now. For instance, a population in Brazilian waters described as *M. scintillae* (Moreira, 1961), was considered likely to be *Phyllorhiza* by later workers (Mianzan and Cornelius, 1999; Silveira and Cornelius, 2000) identification of *Phyllorhiza* (Cutress, 1971). A genetic assessment by Bayha (reported in Bayha and Graham, 2011) of 10 medusae from Laguna Joyuda on the West coast Puerto Rico, which had been earlier morphologically identified as *Mastigias* (Bolton and Graham, 2004) were found to be genetically *Phyllorhiza* for both mitochondrial (cytochrome oxidase subunit III and 16S rRNA) and nuclear (internal transcribed spacer region I, ITS-1 regions). Thus, further studies are necessary to resolve the taxonomic confusion between these two genera. Concerning *Phyllorhiza* sp.2 and sp.3, they may represent new records of species in Malaysian waters that have no reference sequence in GenBank or newly discovered species. Thus, the implication of molecular data on existing taxonomy of *Phyllorhiza* and other jellyfish in general is considerable.

Population genetics investigates the parameters that determine the genetic structure of a population (Halliburton, 2004). It provides valuable infor-

mation for protection and management of species (Kapusinski and Jacobson, 1987; O'Brien, 1994; Frankham, 1995; Fromentin and Powers, 2005). The Australian spotted jellyfish, *P. punctata* is an efficient predator that feeds on zooplankton and fish larvae, consequently affecting the food web of the marine ecosystem, which it inhabits. As such, it can cause serious threat to the fisheries industry and fisheries restoration operation (Ray, 2005c).

This species is reported to be indigenous to the tropical western Pacific Ocean, but has successfully invaded all parts of the world Oceans except the Arctic and Antarctic (Graham *et al.*, 2003). Thus, *P. punctata* is now extensively distributed in the Indo-Pacific Ocean (Chilton *et al.*, 2011; Chuah, 2012), Italian waters and Western Mediterranean (Boero *et al.*, 2009), as well as the Gulf of Mexico (Graham *et al.*, 2003). The appearance of *Phyllorhiza* spp. in the coastal of Malaysia represents, yet another illustration of its invasive ability. Migration of marine fauna (planktonic organism, adults and planktonic larvae of benthic forms) may occur by positive transport of water currents and by other organisms and man; and by active migration for large animals (El-Serehy and Al-Rasheid, 2011).

## Conclusion

Morphological analyses and DNA sequencing based on the present genetic data revealed at least three different species for the genus *Phyllorhiza* and also highlighted that colour alone is not sufficient for species differentiation of *Phyllorhiza* spp. The blue morphotype of *Phyllorhiza* sp.1 observed in the east of Peninsular Malaysia was genetically identical to the brown morphotype observed in Northwest of Peninsular and recognised as *P. punctata* while the presence of *Phyllorhiza* sp.2 and *Phyllorhiza* sp.3 which have never been recorded before in Malaysia. Consequently, understanding the taxonomy of local and invasive jellyfishes are necessary requirements for their management.

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